

FIG. 1A

1 CCTAGAGCCAGCAGAGTCCAGGCTGCTGTTAACAACTTCATGTCCCCGTGGGTAGCAGGC 60  
61 AGGTGCTTCTGTCTGATCTGGCTCCCTTGACCACGTACTCATCAAATAGACCAAGATC 120  
121 CCCAGAGTCCAAGATCCTTACAAGGGGGCCAGAAAGGGATGAGCTTCTGAAGAACACT 180  
181 GATGTAAAATACCAAGGAATTTCACATCGAAGAAGATTTTGATGGCAGCTGGATT 240  
241 GGCCATAATCTAGAACACATGGTAATACAGTTGCAAGTCATTAGTCATATTCTTG 300  
301 CTAAATTGCTGTCTTCAATGGCTGATTGAAGATCCCTTACCCGCCAGGTGCCAAG 360  
361 AACTATGAACAGGCAGGGCAATGAAAGAACACTAAAGAAGGATCCAACGATTGAAATT 420  
421 CCAGAACATTCACTGCTGCAAAAAACAGGTCTGGCCTCGCATCAATAGTGCACAGGCCA 480  
481 GTACAGAGGATGAAACAAGCCTCTCTAGACTGGAAAAGAAACTTGTGAGTCCTGGA 540  
541 TGGAGCAAAAGGCCACAGTGATGACTATGATGACCCCTGAGCTTCGGATGGAAGGAC 600  
601 ATGGCAGTCGATTAAAATTTACCGCCGGCTATAAAGGAATCTGAATATGCAAGATAC 660  
661 ACACATTTCAAGGTTGCAATGGACACTCCCTCCGTTAGACACCAGGACCTCTATCTC 720  
721 CATTGGACAGCCGACCTGGAACACACAGACGAGGTTGAAAGAGTGACAAACCCATTTC 780  
781 CAAGGACGTCAGAACGCAAAACATTAAGGGAGATGCATCGTAAGAAAAGAACAGATTCC 840  
841 TTTACCACCTCCTCGGCCTCTCATAACACTTCCGAGAGTACCAACCCCTGCCCCCTGA 900  
901 GCCGGAGAGCAGCAGGCCACCTTATCTCAGAGACACACCTTCCAGAAGTCCAGAGAA 960  
961 GCCCAGTCAGATAAGCTTAAGGGACTTAAGTGAGGTCTTGAAGCAGAAAAGTCCCTCA 1020  
1021 TAACCAGAGGAAGCCTGAATCAACTCATCTGTTAGAAAACCAAAATACTCAAGAGATTCC 1080  
1081 ACTTGCCATTAGCAGTTCTTCATTCAACGACAAGCAACCACAGTGTGAAACAGAGATCA 1140  
1141 TAGAGGAGGCATGCAGCCCTGTTCTCTCAGAGATGCCAGCCTCCAGCCAGTCAGCCC 1200  
1201 TCACGAAAATATACTGCCCTATAAATACACAAGCTGGAGACCAACCTTCCCCAAAAGGTC 1260  
1261 TGATAGAAAGGATGTCAGCACAAATGAATGGTACATTGGAGAAATACAGCCGCCAGGAGT 1320  
1321 GGAAGAGGCATTGATGAAGGAGAACAGGATGGTAGTTCTGGTCCGAGATTGTTCCAC 1380  
1381 AAAATCCAAGGAAGGCCCTATGTTGGCTGTGTTTATGAGAACAAAGTCTACAATGT 1440  
1441 AAAAATCCGCTTCCTGGAGAGGAATCAGCAGTTGCCCTGGGGACAGGACTCAGAGGAGA 1500

## FIG. 1B

1501 TGAGAAGTTGATTCACTAGAAGACATCATCGAACACTACAAGAATTTCCCATTATACT 1560  
1561 AATTGATGGGAAAGATAAAACTGGGGTCCACAGGAAACAGTGTACCTCACTCAGCCACT 1620  
1621 CCCTCTCACCAAGACACCTCTTGCCTCTGTAGCCCTGGTCCTTGTTATCTTGGTTACT 1680  
1681 GGATTTCAGCGCTTCCATTGTTTCATTGATTCAAAGTTATTTCTGTGCCCTCAAGG 1740  
1741 GACAACCTTTTAACTTGGAGAAAAGAAAAACACTCTATAACAGAGGTGGAAAATCAC 1800  
1801 TCACGGTTTGAAAGTTCAAACCACAGAGAAAATTTATAACATGCAAAA 1851

FIG. 2

FIG. 3A

1	CCTAGAGCCAGCAGAGTCCAGGCTGCTGTTAACAACTTCATGTC	CCCCGGGGTAGCAGGC	60
61	AGGTGCTTCTGTCATCTGGCTCTCCCTGACCAGTACTCATCAA	TAGACCAAGAGATCC	120
121	CCAGAGTCCAAGATCCTAACAGGGGCCAGAAAGGGATGAGCTT	CTGAAGAACAGACT	180
181	GATGTAAGAACAGGAAATTTCATCGAAGAACAGATTTGTGAT	GGCCAGCTGGGATT	240
241	GGCCATAATCTAGAACAGACATGGTGAATACAGTTGCAAGTC	ATTTAGTCATATTC	300
301	CTAAATTGCTGTCTCAATTGGCTGAATTGAGATCCTCTTACCC	CCAGGTGCCAACG	360
1	M A E L K I P L T R Q V P R		14
361	AACATGAAACAGGCCAGGGCAATAGAAAAGACAACAAAGAAGG	ATCCAACGATTGAAATT	420
15	T M N R Q G N R K T T K E G S N D L K F		34
421	CCAGAACITCAGCTGCCCCAAAACAGGTCAATGGCC	TGCGCATCAATAGTGCCACAGGCCA	480
35	Q N F S L P K N R S W P R I N S A T G Q		54
481	GTACCAAGAGGTGAAACAAGCCCTTCTGACTATGGAAAGAAC	TTGCTGCAGTCCTGGA	540
55	Y Q R M N K P L L D W E R N F A A V L D		74
541	TGGAGCAAAAGGCCACAGTGTGACTATGATGACCC	TGAGCTTCGGATGGAAGAAC	600
75	G A K G H S D D D Y D D P E L R M E E T		94
601	ATGGCAGTCGATTAAAATTTTACCGACCCGGCTATAAGGAAT	TCTGAATATGCAAGATAC	660
95	W Q S I K I L P A R P I K E S E Y A D T		114
661	ACACTATTCAAGGTTGCAATGGACACTCCCCTCCGTTAGAC	ACCAGGACCTCTATCTC	720
115	H Y F K V A M D T P L P L D T R T S I S		134
721	CATTGGACAGCCGACCTGGAACACACAGACGAGGTTGAAAGA	GTGGCAAACCCATTTC	780
135	I G Q P T W N T Q T R L E R V D K P I S		154
781	CAAGGACGTCAGAACAGGAAACATTAAAGGAGATGCC	ATCGTAAGAAAAGAACAGATTCC	840
155	K D V R S Q N I K G D A S V R K N K I P		174
841	TTTACCCACCTCTCGGCCTCTCATACACTTCCGAAAGA	GTACCAACCCCTTGCCCCCTGA	900
175	L P P P R P L I T L P K K Y Q P L P P E		194
901	GGCGGAGAGCAGCAGGCCACCTTATCTCAGAGAACAC	CCCTTCCAGAAGTCCAGAGAA	960
195	P E S S R P P L S Q R H T F P E V Q R M		214
961	GCCCAGTCAGATAAGCTTAAGGGACTTAAGTGGAGTCTG	AGAGCAGAAAAAGTTCC	1020
215	P S Q I S L R D L S E V L E A E K V P H		234
1021	TAACCGAGGAAGCTGAATCAACTCATCTGTTAGAAAAC	AAAATACTCAAGAGATTCC	1080
235	N Q R K P E S T H L L E N Q N T Q E I P		254
1081	ACTTGCCATTAGCAGTTCTTCATTCAAGCACAGCAAC	ACAGTGTGCAAAACAGAGATCA	1140
255	L A I S S S F T T S N H S V Q N R D H		274
1141	TAGAGGAGGCATGCAGCCCTGTTCTCTCAGAGATGCCAG	CCTCCAGCCAGCTGCAGCCC	1200

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FIG. 3B

275	R G G M Q P C S P Q R C Q P P A S C S P	294
1201	TCACGAAAATATACTGCCCTATAAAATACACAAGCTGGAGACCCACCTTTCCCCAAAAGTC	1260
295	H E N I L P Y K Y T S W R P P F P K R S	314
1261	TGATAGAAAGGATGTCCAGCACAATGAATGGTACATTGGAGAATACAGCCGCCAGGCAGT	1320
315	D R K D V Q H N E W Y I G E Y S R Q A V	334
1321	GGAAGAGGCATTCAATGAAGGAGAACAAAGGATGGTAGTTCTGGTCCAGAGATTGTTCCAC	1380
335	E E A F M K E N K D G S F L V R D C S T	354
1381	AAAATCCAAGGAAGAGCCCTATGTTTGGCTGTGTTTATGAGAACAAAGTCACAAATGT	1440
355	K S K E E P Y V L A V F Y E N K V Y N V	374
1441	AAAAATCCGCTTCCTGGAGAGGAATCAGCAGTTGCCCTGGGACAGGACTCAGAGGAGA	1500
375	K I R F L E R N Q F A L G T G L R G D	394
1501	TGAGAAAGTTGATTCAGTAGAACATCATCGAACACTAACAGAATTTCCTTCCATTATACT	1560
395	E K F D S V E D I I E H Y K N F P I I L	414
1561	AATTGATGGAAAGATAAAACTGGGGTCCACAGGAACAGTGTCACCTCACTCAGCCACT	1620
415	I D G K D K T G V H R K Q C H L T Q P L	434
1621	CCCTCTCACAGACACCTTGCCTCTGTAGCCTGGCTTTGTGTTATCTTGGTTTACT	1680
435	P L T R H L L P L *	444
1681	GGATTCAAGCGCTTCCATTGTTTCATTGATTCAAAAGTTATTTCTGTGCCCTCAAGG	1740
1741	GACAACCTTTTAACTTGGAGAAAAGAAAAACACTCTATAACAGAGGTGAAAATCAC	1800
1801	TCACGGTTTGAAAGTCAAACACAGAGAAAATATTATAACATGCAAAA	1851

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**FIG. 4A**

1 GTCAGACCTCTCAGGTCTGGCTGCATTTCACAGGAAACCAAGTCTAAAACGGACCTAT 60  
61 CAGGAGGTTTCTGCTGAAGGGCACTGCTTAGCATCGAGAAGAATTCAACCACCCCTT 120  
121 ACTAATTCCAGTCCCCAAGGTCTCTGCACTGCCGCCCTCCTCACAGGAGACGGACAC 180  
181 CTCAGCCTAGATCCCTGGTGCTCCACGCTGTTAGCTGAATTGAAGATCCCTTTA 240  
241 CCCGCCAGGTGCCAGAACATGACAGGCAGGGCAATAGAAAAGACAACATAAGAAGGAT 300  
301 CCAACGATTGAAATTCCAGAACATTCAGTCTGCCAAAAAACAGGTCTGGCCTCGATCA 360  
361 ATAGTGCCACAGGCCAGTACCAAGAGGATGAACAAGCCTCTTAGACTGGAAAGAAACT 420  
421 TTGCTGCAGTCCTGGATGGAGCAAAGGCCACAGTGATGATGACTATGATGACCCCTGAGC 480  
481 TTCCGATGGAAGAGACATGGCAGTCGATTAACCTTACAGCCGCCCTATAAAGGAAT 540  
541 CTGAATATGCAGATAACACTATTCAGGTTGCAATGGACACTCCCTCGITAGACA 600  
601 CCAGGACCTCTATCCATTGGACAGCCGACCTGGAACACACAGACGAGGTTGGAAAGAG 660  
661 TGGACAAACCCATTCCAAGGACGTCAGAACGCAAACATTAAGGAGATGCATCCGTAA 720  
721 GAAAGAACAGATTCCCTTACCACTCCTCGGCCTCTCATACACTCCGAAGAACAGTACC 780  
781 AACCTTGCCCCCTGAGCCGGAGAGCAGCAGGCCACCTTATCTCAGAGACACACCTTTC 840  
841 CAGAAGTCCAGAGAACGCCCAGTCAGATAAGCTTAAGGACTTAAGTGAGGCTTGAAAG 900  
901 CAGAAAAAGTCCCTCATAACAGAGGAAGCCTGAATCAACTCATCTGTTAGAAAACAAA 960  
961 ATACTCAAGAGATTCCACTTGCCATTAGCAGTCTTCATTCAAGAACAGCAACCACAGTG 1020  
1021 TGCAAAACAGAGATCATAGAGGAGCATGCAGCCCTGTTCTCCAGAGATGCCAGCCTC 1080  
1081 CAGCCAGCTGCAGCCCTCACGAAAATATACTGCCCTATAAAACACAGCTGGAGACCAC 1140  
1141 CTTTCCCCAAAGGTCTGATAGAAAGGATGTCCAGCACAATGAATGGTACATTGGAGAAT 1200  
1201 ACAGCCGCCAGGCACTGGAGAGGCAATTGAGAAGGAGAACAGGATGGTAGTTCTGG 1260  
1261 TCCGAGATTGTCACAAAATCCAAGGAAGAGGCCATTGTTGGCTGTGTTTATGAGA 1320  
1321 ACAAAAGTCTACAATGAAAAATCCGCTTCCGGAGAGGAATCAGCAGTTGCCCTGGGA 1380  
1381 CAGGACTCAGAGGAGATGAGAAGTTGATTCACTGAGAACATCATCGAACACTACAAGA 1440

## FIG. 4B

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1441	ATTTCCCATTATACTAATTGATGGAAAGATAAAACTGGGTCCACAGGAAACAGTGTC	1500
1501	ACCTCACTCAGCCACTCCCTCTCACAGACACCTTGCCTCTGTAGCCTGGCTTTGTG	1560
1561	TTATCTTGGTTACTGGATTAGCGCTTCCATTGTTTCAATTGATTCAAAAGTTTATT	1620
1621	TTCTGTGCCCTCAAGGGACAACCTTTTAACCTTGAGAAAAGAAAAACACTCTATAACA	1680
1681	GAGAGTGGAAAATCACTACGGTTTGAAAGTTCAAACCACAGAGAAAATTTATAACA	1740
1741	TGCAAAAAATAAAACATTCTAGTAACTGGCCACTGGAAAATAAATAAAATAAAACTA	1800
1801	GGGTTTAAAGTATCTCTAAAAAACAAACAACAAAAACTATATAAACATAGCCATTAT	1860
1861	GCTCATGATACAGGGAGCAGCAAGGGCACCAGAAGCTGTTGCTTAAATGTTGCAGTC	1920
1921	AGTGCAAGACAAGTCTATGGGAAATCCCAAATCTGTGCTTTACAGGACACTGCGCTG	1980
1981	CCTTTATGTCAGTTGGCCTTACATATATAACATGTGTTGATGATTCTTACACTAA	2040
2041	AGATGCTGGGCTGGGTGCGGTGCCTCATGCCGTAACTCCAGCACTTGGGAGGCTGAGG	2100
2101	TGGACAGATCACGAGCTCAGGAGATCAAGACCATCCTGGCTAACATGGTGAACCCCCATG	2160
2161	TCTACTAAAATAACAAAAATCAGCTGGCGTGGTGGTGGGTGCCCTGTAGTCCCAGCTAC	2220
2221	TCGGGAGGCTGAGGCAGGAGAATGGTGTGAACCCGGGAGGCGGAGCTGCAGTGAGCCGA	2280
2281	AATCGCGCCACTGCACTCCAATCCAGCCTGGGACAGAGAGACTCCGTCCTCAAA	2335

FIG. 5

1	M	N	R	Q	G	N	R	K	T	T	K	E	G	S	14
15	N	D	L	K	F	Q	N	F	S	L	P	K	N	R	34
35	S	A	T	G	Q	Y	Q	R	M	N	K	P	L	L	54
55	A	A	V	L	D	G	A	K	G	H	S	D	D	D	74
75	R	M	E	E	T	W	Q	S	I	K	I	L	P	A	94
95	E	Y	A	D	T	H	Y	F	K	V	A	M	D	T	114
115	R	T	S	I	S	I	G	Q	P	T	W	N	T	Q	134
135	D	K	P	I	S	K	D	V	R	S	Q	N	I	K	154
155	K	N	K	I	P	L	P	P	P	R	P	L	I	T	174
175	P	L	P	P	E	P	E	S	S	R	P	P	L	S	194
195	E	V	Q	R	M	P	S	Q	I	S	L	R	D	L	214
215	E	K	V	P	H	N	Q	R	K	P	E	S	T	H	234
235	T	Q	E	I	P	L	A	I	S	S	S	S	F	T	254
255	Q	N	R	D	H	R	G	G	M	Q	P	C	S	P	274
275	A	S	C	S	P	H	E	N	I	L	P	Y	K	T	294
295	F	P	K	R	S	D	R	K	D	V	Q	H	N	E	314
315	S	R	Q	A	V	E	E	A	F	M	K	E	N	K	334
335	R	D	C	S	T	K	S	K	E	E	P	Y	V	L	354
355	K	V	Y	N	V	K	I	R	F	L	E	R	N	Q	374
375	G	L	R	G	D	E	K	F	D	S	V	E	D	I	394
395	F	P	I	I	L	I	D	G	K	D	K	T	G	V	414
415	L	T	Q	P	L	P	L	T	R	H	L	L	P	L	428

FIG. 6A

1	GTCAGACCTCTCAGGCTGTGGCTGCATTTCACAGGAAACCAAGTCTAAAACGGACCTAT	60
61	CAGGAGGTTTCTGCTGAAGGGCACTGCTTAGCATCGAGAAGAATTCAACCCACCGCCTT	120
121	ACTAATTCCAGTGCCCAAGGTCTGCACTGCCGCCCTCCACAGGAGACGGACAC	180
181	CTCAGCCTAGATCCCTGGTCTCCACGCTGTCAGGCTGAATTGAAGATCCCTCTTA	240
241	CCCGCCAGGTGCCAAGAACCTATGAAACAGGCAGGGCAATAGAAAAGACAACCTAAAGAAGGAT	300
1	M N R Q G N R K T T K E G S	14
301	CCAACGATTGAAATTCCAGAACCTTCAGTCTGCCAAAAAACAGGTATGGCTCGCATCA	360
15	N D L K F Q N F S L P K N R S W P R I N	34
361	ATAGTGCACAGGCCAGTACCCAGAGGATGAAACAGCCTCTCTAGACTGGAAAGAAAAC	420
35	S A T G Q Y Q R M N K P L L D W E R N F	54
421	TTGCTGCAGTCCTGGATGGACCAAAGGCCACAGTGATGATGACTATGATGACCCCTGAGC	480
55	A A V L D G A K G H S D D D Y D D P E L	74
481	TTGGATGGAAGAGACATGGCAGTCGATTAATTTACAGCCGGCTATAAGGAAT	540
75	R M E E T W Q S I K I L P A R P I K E S	94
541	CTGAATATCAGACATACACTATTCAAGGTTGCAATGGACACTCCCCCTCCGTTAGACA	600
95	E Y A D T H Y F K V A M D T P L P L D T	114
601	CCAGGACCTCTATCCATTGGACAGCCGACCTGGAACACACAGACGAGGTTGAAAGAG	660
115	R T S I S I G Q P T W N T Q T R L E R V	134
661	TGGACAAACCATTCCAAGGACGTCAGAACAGCAAAACATTAAAGGAGATGCATCCGTA	720
135	D K P I S K D V R S Q N I K G D A S V R	154
721	GAAAGAACAGATTCTTACCCACTCTCGGCCTCTCATAACACTTCCGAAGAAGTACC	780
155	K N K I P L P P P R P L I T L P K K Y Q	174
781	AACCCCTGCCCCCTGAGCCGGAGAGCAGCAGGCCACCTTATCTCAGAGACACACCTTC	840
175	P L P P E P E S S R P L P S Q R H T F P	194
841	CAGAAAGTCCAGAGAACATGCCAGTCAGATAAGCTTAAGGGACTTAAGTGAGGCTCTGAAG	900
195	E V Q R M P S Q I S L R D L S E V L E A	214
901	CAGAAAAAGTCTCTCATAAACCAGAGGAAGCCCTGAATCAACTCATCTGTTAGAAAACCAA	960
215	E K V P H N Q R K P E S T H L L E N Q N	234
961	ATACTCAAGAGATTCCACTTGCCATTAGCAGTTCTCATTCAAGCACAACAGTG	1020
235	T Q E I P L A I S S S S F T T S N H S V	254
1021	TGCAAAACAGAGATCATAGAGGAGGCATGCAGCCCTGTTCTCCTCAGAGATGCCAGCCTC	1080
255	Q N R D H R G G M Q P C S P Q R C Q P P	274
1081	CAGCCAGCTGCAGGCCCTCACGAAAAATACTGCCCTATAAATACACAAGCTGGAGACCA	1140
275	A S C S P H E N I L P Y K Y T S W R P P	294

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FIG. 6B

1141	CTTCCCCAAAAGGTCTGATAGAAAGGATGTCCAGCACAATGAATGGTACATTGGAGAAT	1200
295	F P K R S D R K D V Q H N E W Y I G E Y	314
1201	ACAGCCGCCAGGCAGTGGAGAGGCAATTGATGAGGAGAACAGGTGGTAGTTCTTG	1260
315	S R Q A V E E A F M K E N K D G S F L V	334
1261	TCCGAGATTGTTCCACAAAATCCAAGGAAGAGCCCTATGTTGGCTGTGTTTATGAGA	1320
335	R D C S T K S K E E P Y V L A V F Y E N	354
1321	ACAAAGTCTACAATGAAAAATCGCTTCCTGGAGAGGAATCAGCAGTTGCCCTGGGA	1380
355	K V Y N V K I R F L E R N Q Q F A L G T	374
1381	CAGGACTCAGAGGAGATGAGAAAGTTGATTCACTAGAGAACATCATCGAACACTACAAGA	1440
375	G L R G D E K F D S V E D I I E H Y K N	394
1441	ATTTTCCCATTACTAATTGATGGAAAGATAAAACTGGGGTCCACAGGAAACAGTGT	1500
395	F P I I L I D G K D K T G V H R K Q C H	414
1501	ACCTCACTCAGCCACTCCCTCACCGACACCTCTGGCTCTGTAGCTGGTCTTGTG	1560
415	L T Q P L P L T R H L L P L	429
1561	TTATCTTGGTTTACTGGATTCA CGCCTTCATTGTTTCA TTGATTTCAAAGTTTATT	1620
1621	TTCTGTGCCCTCAAGGGACAAC TTTTAACTTTGGAGAAAAGAAAACACTCTATAACA	1680
1681	GAGAGTGGAAAATCACTCACGGTTTGGAAAGTTCAAAACCACAGAGAAAATITATAACA	1740
1741	TGCAAAAATAAAACATTCTAGTA CTGGCACTGGAAAATAAATAAAAATAAAACTA	1800
1801	GGTTTTAAAAGTATCTTCTAAAACAAACAAAAAAACTATATAACATAGCCATTAT	1860
1861	GCTCATGATACAGGGAGCAGCAAAAGGGCACAGAACAGTGTGCTTAAATGTTGCAGTC	1920
1921	AGTGCAAGACAAGTCTATGGGAAATCCCAATCTGTCTTCACTGGACACTGCCTG	1980
1981	CCTTATGTCAGTTGGCCTTACATATATACATGTGTGGATGATTCTTACACTAA	2040
2041	AGATGCTGGGCTGGTGCAGGCTCATGCCTGTAATCCAGCACTTGGAGGCTGAGG	2100
2101	TGGACAGATCACGAGGTCAAGGAGATCAAGACCATCTGGCTAACATGGTGAACCCCATG	2160
2161	TCTACTAAAATACAAAAAAATCAGCTGGGGCTGGTGGGGTGCCTGTAGTCCCAGCTAC	2220
2221	TCGGGAGGCTGAGGCAGGAGAATGGTGAACCCGGAGGGAGCTGAGCCGA	2280
2281	AATCGCGCCACTGCACCCAATCCAGCCTGGGACAGAGAACCTCGTCTCAAA	2335

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# FIG. 7A

1	GGCTGCTGTTAACAACTCATGCCCCGTGGTAGCAGGCAGGTGCTCTGTCTGATCTG	60
61	GCTCTCCTGACCACGTACTCATCAAATAGACCAAGATCCCCAGAGTCCAAGATCCTTA	120
121	CAAGGGGCCAGAAAGGGTAGCTGAGAAGACTGATGTAAAATACCAGGAATT	180
181	TTGACATCGAAGAAGATTGTGATGGCAGCTGGGATTGGCCATAATCTAGAACAC	240
241	ATGGTGAATACAGTGCAGTCATTAGTCATATTCTTGCTAAATTGCTGTCTCAA	300
301	TGGGGCAATAGAAAGACAACAACTAAAAGAGATCCAACGATTGAAATTCCAGAACACTCAGT	360
361	CTGCCAAAAAACAGGTATGGCCTCGCATCAATAGTCCCACAGGCCAGTACAGAGGATG	420
421	AACAAGCCTCTCTAGACTGGATTGGCAGCTTGACCATTATTATCGCACAGTGGATGC	480
481	AATCAGAAGCTGGCACAGCATGGCTCAACTAGTCCCCTGTTCTGGTCTCACAAAGAC	540
541	TGAAAGCAACATGCTGGCAGGGCTGCATTCTCCTCCAGGGCTCTGAAGAGGAACCTGCT	600
601	TCCAGATTCTTCAGGAAAGAAAACTTGCTGCACTGGATGGAGCAAAAGGCCACAGT	660
661	GATGATGACTATGATGACCCCTGAGCTCGATGGAAGAGACATGGCAGTCATTAAATT	720
721	TTACCCAGCCGGCTATAAGGAATCTGAATATGCAAGACACACTATTCAGGTTGCA	780
781	ATGGACACTCCCCCTCCGTTAGACACCCAGGACCTCTATCTCATTGGACAGCCGACCTGG	840
841	AACACACAGACGAGGTTGGAAAGACTGGACAAACCCATTCCAAGGAGCTCAAGCCAA	900
901	AACATTAAAGGAGATGCATCCGTAAGAAAAGAACAAAGATTCTTACCCACCTCTCGCC	960
961	CTCATAACACTTCCGAAGAAGTACCAACCCCTGCCCCCTGAGCCGGAGAGCAGGCCA	1020
1021	CCTTTATCTCAGAGACACACCTTCCAGAAGTCCAGAGAATGCCAGTCAGATAAGCTTA	1080
1081	AGGGACTTAAGTGAGGCCTTGAAGCAGAAAAAGTCCCTCATACCAGAGGAAGCCTGAA	1140
1141	TCAACTCATCTGTTAGAAAACCAAAACTCAAGAGATTCCACTTGCCTTAGCAGTTCT	1200
1201	TCATTACGACAAGCAACCACAGTGTGCAAAACAGAGATCATAGAGGAGGCATGCAGCCC	1260
1261	TGTTCTCCTCAGAGATGCCAGCCTCCAGCCAGCTGAGCCCTCACAAAATATACTGCC	1320
1321	TATAAAATACACAAGCTGGAGACCACCTTCCAAAAGGCTGATAGAAAGGATGTCAG	1380
1381	CACAATGAATGGTACATTGGAGAACATAGCCGCCAGGCAGTGGAAAGAGGCATTGAG	1440

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## FIG. 7B

1441 GAGAACAAAGGATGGTAGTTCTTGGTCCGAGATTGTTCCACAAAATCCAAGGAAGAGCCC 1500  
1501 TATGTTTGGCTGTGTTTATGAGAACAAAGTCTACAATGTAAAAATCCGCTTCCTGGAG 1560  
1561 AGGAATCAGCAGTTGCCCTGGGGACAGGACTCAGAGGAGATGAGAAGTTGATTCACTA 1620  
1621 GAAGACATCATCGAACACTACAAGAATTTCCTTCAATTACTAATTGATGGAAAGATAAA 1680  
1681 ACTGGGGTCCACAGGAAACAGTGTACCTCACTCAGCCACTCCCTCTCACAGACACCTC 1740  
1741 TTGCCTCTGTAGCCTGGCTTGTGTTATCTTGTTACTGGATTCAAGCGCTTCATTG 1800  
1801 TTTTCATTGATTCAAAAGTTATTTCCTGTGCTTCAAGGGACAACTTTTTAACTTG 1860  
1861 GAGAAAAGAAAAACACTCTATAACAGAGAGTGGAAAATCACTCACGGTTTGAAAGTCA 1920  
1921 AACACAGAGAAAATTTATAACATGAAAAAATAAAACATTCTAGTAACGGCCACT 1980  
1981 GGAAAATAAATAAAAATAAAACTAGGGTTTAAAGTATCTCTAAAAACACAA 2040  
2041 AAAACTATAAACATAGCCATTATGCTCATGATAACAGCGAGCAGCAAAGGGCACCAGA 2100  
2101 AGCTGTTGCTTAAATGTTGCAGTCAGTGCAAGACAAGTCTATGGAAATTCCCAAATCT 2160  
2161 GTGCTCTTACAGGACACTGCGCTGCCCTTATGTCAGTTGGCCTTACATATATACA 2220  
2221 ATGTGTGGATGATTCTTACACTAAAGATGCTGGCTGGGTGCGGTGCCTCATGCCGTGA 2280  
2281 ATCCCAGCACTTGGGAGGCTGAGGTGGACAGATCACGAGGTCAAGGAGATCAAGACCATC 2340  
2341 CTGGCTAACATGGTAAACCCCCATGTCATAAAAATACAAAAAATCAGCTGGCGTGGT 2400  
2401 GGTGGGTGCCTGTAGTCCCAGCTACTCGGGAGGCTGAGGCAGGAGAATGGTGTGAACCCG 2460  
2461 GGAGGCGGAGCTGCAGTGAGCCGAAATCGCGCCACTGCACTCCAATCCAGCCTGGGAC 2520  
2521 AGAGAGACTCCGTCTCAAAA 2540

FIG. 8

1		M	E	E	T	W	Q	S	I	K	I	10									
11	L	P	A	R	P	I	K	E	S	E	Y	A	D	T	H	Y	F	K	V	A	30
31	M	D	T	P	L	P	L	D	T	R	T	S	I	S	I	G	Q	P	T	W	50
51	N	T	Q	T	R	L	E	R	V	D	K	P	I	S	K	D	V	R	S	Q	70
71	N	I	K	G	D	A	S	V	R	K	N	K	I	P	L	P	P	P	R	P	90
91	L	I	T	L	P	K	K	Y	Q	P	L	P	P	E	P	E	S	S	R	P	110
111	P	L	S	Q	R	H	T	F	P	E	V	Q	R	M	P	S	Q	I	S	L	130
131	R	D	L	S	E	V	L	E	A	E	K	V	P	H	N	Q	R	K	P	E	150
151	S	T	H	L	L	E	N	Q	N	T	Q	E	I	P	L	A	I	S	S	S	170
171	S	F	T	T	S	N	H	S	V	Q	N	R	D	H	R	G	G	M	Q	P	190
191	C	S	P	Q	R	C	Q	P	P	A	S	C	S	P	H	E	N	I	L	P	210
211	Y	K	Y	T	S	W	R	P	P	F	P	K	R	S	D	R	K	D	V	Q	230
231	H	N	E	W	Y	I	G	E	Y	S	R	Q	A	V	E	E	A	F	M	K	250
251	E	N	K	D	G	S	F	L	V	R	D	C	S	T	K	S	K	E	E	P	270
271	Y	V	L	A	V	F	Y	E	N	K	V	Y	N	V	K	I	R	F	L	E	290
291	R	N	Q	Q	F	A	L	G	T	G	L	R	G	D	E	K	F	D	S	V	310
311	E	D	I	I	E	H	Y	K	N	F	P	I	I	L	I	D	G	K	D	K	330
331	T	G	V	H	R	K	Q	C	H	L	T	Q	P	L	P	L	T	R	H	L	350
351	L	P	L																		353

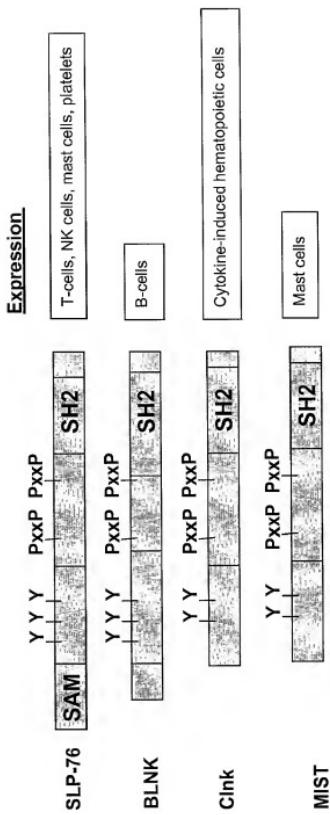
FIG. 9A

1	GGCTGCTGTTAACAACTTCATGTCCCCGTGGGTAGCAGGCAGGTGCTTGTGATCTG	60
61	GCTCTCCCTTGACCACTGTACTCATCAAATAGACCAAGATCCCCAGAGTCCAAGATCCTTA	120
121	CAAGGGGCCAGAAAGGGTAGAGCTTCTGAAGAACACTGTGATAAAATACCAGGAATT	180
181	TTGACATCGAAGAAGATTGATGGCAGTGGGATTGGCCATAATCTACAAGACAC	240
241	ATGGTGAATACAGTTGCAAGTCATITAGTCATATTCTGCTAAATTGCTGTOTCTTCAA	300
301	TGGGCAATAGAAAAGACAACAAAGAAGGATCCAACGATTGAAATTCCAGAACATTCACTG	360
361	CTGCCAAAAAACAGGTCATGGCCTCCATCAAATAGTCCCACAGGCCAGTACCAAGGGATG	420
421	AACAAAGCCTTCTAGACTGGATTGGCAGCTTGACCATTATTATCGCACAGTGGATGC	480
481	AATCAGAAGTCTGGGACACAGCATGGCTCAACTAGTCCCTGTTCTGGGCTCAACAGAC	540
541	TGAAAGCACATGCTGGCAGGGCTGATTCTCCTCCAGGGGCTCTGAAGAGGAACTTGCT	600
601	TCCAGATTCTTCAGGAAAAGAAACTTGTGCTGCAGTCTGGATGGAGCAAAGGCCACAGT	660
661	GATGATGACTATGATGACCCCTGAGCTTCGGATGGAAGAGACATGGCAGTCGATTAAATT	720
1	M E E T W Q S I K I	10
721	TTACCGCCGGCTATAAAGGAATCTGAATATGCAAGATAACACACTATTCAAGGTTGCA	780
11	L P A R C I K E S E Y A D T H Y F K V A	30
781	ATGGACACTCCCCCTCCGTTAGACCCAGGACCTCTATCTCCATTGGACAGCCGACCTGG	840
31	M D T P L P L D T R T S I S I G Q P T W	50
841	AACACACAGCAGGAGTTGGAAAAGAGTGGACAAACCCATTCCAAAGGACGTCAAGAGCCAA	900
51	N T Q T R L E R V D K P I S K D V R S Q	70
901	AACATTAAAGGAGATGCATCGTAAGAAAGAACAAAGATTCTTACACCTCCTOGGCCT	960
71	N I K G D A S V R K N K I P L P P P R P	90
961	CTCATACACTCCGAAAGAAGTACCAACCCCTGGCCCTGAGCCGGAGAGCAGCAGGCCA	1020
91	L I T L P K K Y Q P L P P E P E S S R P	110
1021	CCTTATCTCAGAGACACACCTTCCAGAAGTCCAGAGAATGCCAGTCAGATAAGCTTA	1080
111	P L S Q R H T F P E V Q R M P S Q I S L	130
1081	AGGGACTTAAGTGAGGTCTTGAAGCAGAAAAAGTCCCTCATAACAGAGGAAGCCTGAA	1140
131	R D L S E V L E A E K V P H N Q R K P E	150
1141	TCAACTCATCTGTTAGAAAACCACAAACTCAAGAGATTCCACTTGCCATTAGCAGTTCT	1200
151	S T H L L E N Q N T Q E I P L A I S S S	170
1201	TCATTACGACAAGCAACCACAGTGTGCAAAACAGAGAGTATAGAGGGGGCATGCAGGCC	1260
171	S F T T S N H S V Q N R D H R G G M Q P	190
1261	TGTTCTCCTCAGAGATGCCAGCCTCCAGCCAGCTGCAAGCCCTCACGAAAATACTGCC	1320

FIG. 9B

191	C	S	P	Q	R	C	Q	P	P	A	S	C	S	P	H	E	N	I	L	P	210
1321	TATAAA	TACACA	AGCTGGAGACCAC	CTT	CCCCAAA	AGGTCTGATAGAA	AGGATGTCCAG														1380
211	Y	K	Y	T	S	W	R	P	P	F	P	K	R	S	D	R	K	D	V	Q	230
1381	CA	CAATGA	TGGTACATTGG	GAGAAT	ACAGCCGCCAGGC	AGCTGGAA	AGAGGCATT	CATGAA													1440
231	H	N	E	W	Y	I	G	E	Y	S	R	Q	A	V	E	E	A	F	M	K	250
1441	GAGAAC	AAAGGATGGTAGTTCTTG	GGCAGAGATTG	TTC	CCAA	AAATCCAAGG	AAAGAGCCC														1500
251	E	N	K	D	G	S	F	L	V	R	D	C	S	T	K	S	K	E	E	P	270
1501	TATGTTT	GGCTGTGTTTATGAGA	ACAAAGTCTACAA	ATGTA	AAA	ATCCGTT	CCTGGAG														1560
271	Y	V	L	A	V	F	Y	E	N	K	V	Y	N	V	K	I	R	F	L	E	290
1561	AGGAATC	AGCAGTTGCCCTGGG	ACAGGACTCAGAGG	AGATGAGA	AGTTGATT	CAGTA															1620
291	R	N	Q	F	A	L	G	T	G	L	R	G	D	E	K	F	D	S	V	310	
1621	GAAGACAT	CATCGAACACTACA	AGAATT	TTTCC	CATTATA	CTACTA	ATTGATG	GGAAAGATA													1680
311	E	D	I	I	E	H	Y	K	N	F	P	I	I	L	I	D	G	K	D	K	330
1681	ACTGGG	TGCCAACAGGAA	ACAGTGT	CACCTCA	CTCAG	GGCCACT	CCCTCTCAC	CCAGACAC	CTC												1740
331	T	G	V	H	R	K	Q	C	H	L	T	Q	P	L	P	L	T	R	H	L	350
1741	TTGCC	CTCTGAGCTGG	TCTTGTGTT	ACTG	TTGTT	ACTGG	ATT	CAGCG	CTTC	CATTG											1800
351	L	P	L	*																	354
1801	TTTCATTG	ATTCAAAG	TTTATTCTGT	GCGCTTCA	AGGG	ACA	ACT	TTT	TTA	ACT	TTG										1860
1861	GAGAAA	AGAAAAAC	ACTCTATA	ACAGAG	AGTGG	AAAAT	ACTC	ACG	TTT	GAA	AGTTCA										1920
1921	AACCACAG	AGAAAAT	ATTTATA	ACATGC	AAA	AAA	AA	AC	TTCTAG	TA	ACTGCC	ACT									1980
1981	GGAAA	ATAA	AAAAA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA		2040
2041	AAA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA	AA		2100
2101	AGCTG	TGCTTAA	ATGTTG	CAGTC	AGTGC	AA	AGCA	AC	ATG	T	ATGG	AA	AT	CC	AA	AT	CT				2160
2161	GTG	CTTTACAGG	ACACT	CGCG	CTGCC	TTATG	TG	CAG	TTG	TTGG	CC	TTAC	AT	AT	AT	AC	AT				2220
2221	ATG	TG	GGATG	ATT	CTTAC	ACTAA	AGATG	C	TGGG	CTGGG	TGCGG	TGCT	CAT	G	C	TG					2280
2281	ATCCC	AGCA	CTTTGG	GAGG	GCTG	AGGTGG	ACAGAT	CAC	GAGG	TG	CAGG	AGAT	CA	AG	AC	ATC					2340
2341	CTGG	CTAACATGG	TGA	AAACCC	CATG	TCTACT	AAA	ATC	AAA	AA	ATC	AGCT	TG	GG	CG	TG					2400
2401	GGTGG	GTGCTG	TAGT	CCCAG	T	ACTCG	GGG	AGG	GCTG	AGG	GAGG	GAGA	AT	GGT	TG	GA	ACCCG				2460
2461	GGAGG	CGGGAGCTT	CGAGT	GAGCC	GA	ATCG	CGC	CC	ACTG	C	ACT	CC	AA	TCC	AGC	CT	GGG	GAC		2520	
2521	AGAGAGA	CTCG	TCTC	AAAA																	2540

FD9260-55699660



**FIG. 10**

**FIG. 11**  
**Recombinant MIST proteins**

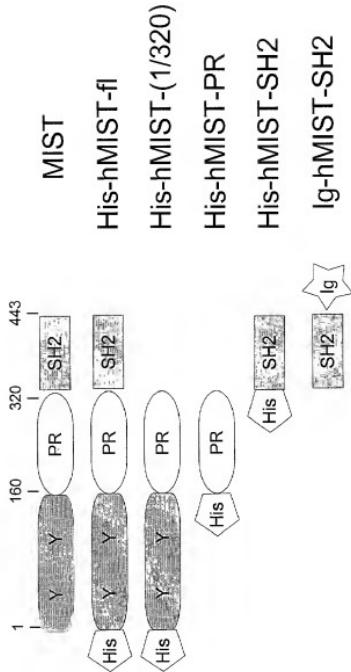
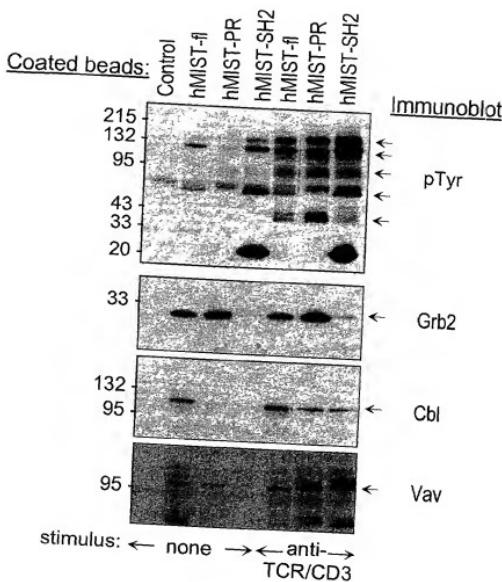
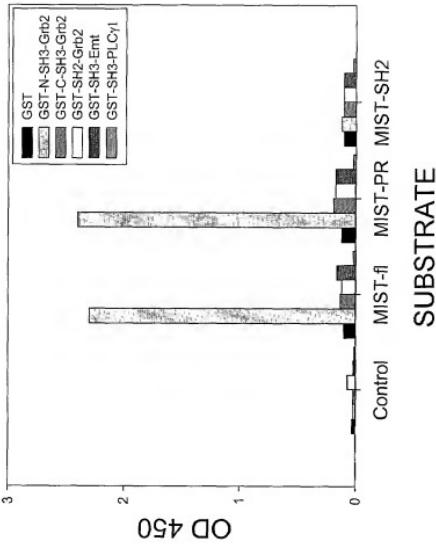


FIG. 12



**FIG. 13**  
**Interaction between hMIST and Grb2-SH3 domain**



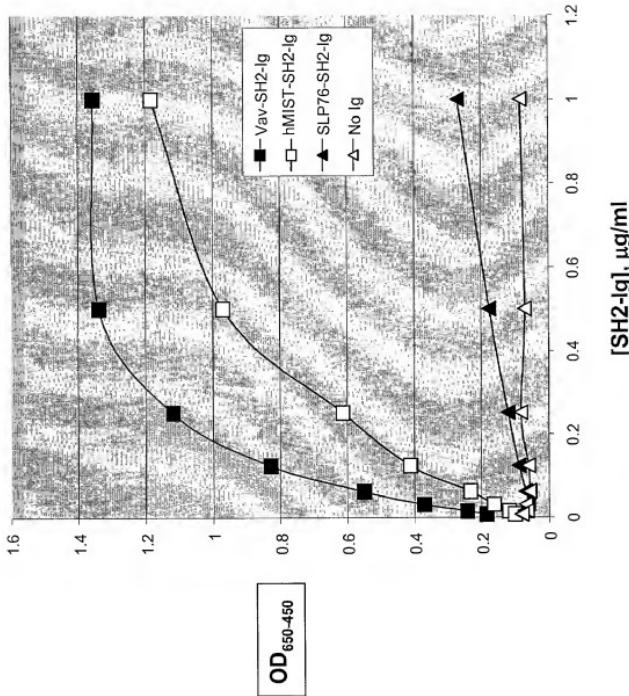
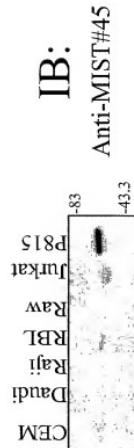


FIG. 14

0996655 0996601

**FIG. 15A**



pervanadate

